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SEQUENCE LISTING

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Malik, Asrar B.  
Pulido, Jose S.

<120> SILENCING OF TGF-BETA TYPE II RECEPTOR EXPRESSION BY siRNA

<130> UIC0005US.NP

<150> US 60/495,161  
<151> 2003-08-13

<150> US 60/517,809  
<151> 2003-11-06

<150> US 60/561,542  
<151> 2004-04-09

<150> PCT/US2004/025984  
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 gtgcagcttc cctcggccgc cgggggcctc cccgcgcctc gccggccctcc aggccccctcc 180  
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 tccggagagg gcgcggcgcg gagcgcagcc aggggtccgg gaaggcgccg tccgtgcgct 300  
 gggggctcgg tctatgacga gcagcggggt ctgcc atg ggt cgg ggg ctg ctc 353  
 Met Gly Arg Gly Leu Leu  
 1 5

agg ggc ctg tgg ccg ctg cac atc gtc ctg tgg acg cgt atc gcc agc 401  
 Arg Gly Leu Trp Pro Leu His Ile Val Leu Trp Thr Arg Ile Ala Ser  
 10 15 20

acg atc cca ccg cac gtt cag aag tcg gtt aat aac gac atg ata gtc 449  
 Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val  
 25 30 35

act gac aac aac ggt gca gtc aag ttt cca caa ctg tgt aaa ttt tgt 497  
 Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys  
 40 45 50

gat gtg aga ttt tcc acc tgt gac aac cag aaa tcc tgc atg agc aac 545  
 Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn  
 55 60 65 70

tgc agc atc acc tcc atc tgt gag aag cca cag gaa gtc tgt gtg gct 593  
 Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala  
 75 80 85

gta tgg aga aag aat gac gag aac ata aca cta gag aca gtt tgc cat 641  
 Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His  
 90 95 100

gac ccc aag ctc ccc tac cat gac ttt att ctg gaa gat gct gct tct 689  
 Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser  
 105 110 115

cca aag tgc att atg aag gaa aaa aaa aag cct ggt gag act ttc ttc 737  
 Pro Lys Cys Ile Met Lys Glu Lys Lys Pro Gly Glu Thr Phe Phe  
 120 125 130

atg tgt tcc tgt agc tct gat gag tgc aat gac aac atc atc ttc tca Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asn Ile Ile Phe Ser 135 140 145 150	785
gaa gaa tat aac acc agc aat cct gac ttg ttg cta gtc ata ttt caa Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Val Ile Phe Gln 155 160 165	833
gtg aca ggc atc agc ctc ctg cca cca ctg gga gtt gcc ata tct gtc Val Thr Gly Ile Ser Leu Leu Pro Pro Leu Gly Val Ala Ile Ser Val 170 175 180	881
atc atc atc ttc tac tgc tac cgc gtt aac cgg cag cag aag ctg agt Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn Arg Gln Gln Lys Leu Ser 185 190 195	929
tca acc tgg gaa acc ggc aag acg cgg aag ctc atg gag ttc agc gag Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys Leu Met Glu Phe Ser Glu 200 205 210	977
cac tgt gcc atc atc ctg gaa gat gac cgc tct gac atc agc tcc acg His Cys Ala Ile Ile Leu Glu Asp Asp Arg Ser Asp Ile Ser Ser Thr 215 220 225 230	1025
tgt gcc aac aac atc aac cac aca gag ctg ctg ccc att gag ctg Cys Ala Asn Asn Ile Asn His Asn Thr Glu Leu Leu Pro Ile Glu Leu 235 240 245	1073
gac acc ctg gtg ggg aaa ggt cgc ttt gct gag gtc tat aag gcc aag Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala Lys 250 255 260	1121
ctg aag cag aac act tca gag cag ttt gag aca gtg gca gtc aag atc Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys Ile 265 270 275	1169
ttt ccc tat gag gag tat gcc tct tgg aag aca gag aag gac atc ttc Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys Thr Glu Lys Asp Ile Phe 280 285 290	1217
tca gac atc aat ctg aag cat gag aac ata ctc cag ttc ctg acg gct Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr Ala 295 300 305 310	1265
gag gag cgg aag acg gag ttg ggg aaa caa tac tgg ctg atc acc gcc Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr Ala 315 320 325	1313
ttc cac gcc aag ggc aac cta cag gag tac ctg acg cgg cat gtc atc Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val Ile 330 335 340	1361
agc tgg gag gac ctg cgc aag ctg ggc agc tcc ctc gcc cg ggg att Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser Ser Leu Ala Arg Gly Ile 345 350 355	1409

gct cac ctc cac agt gat cac act cca tgt ggg agg ccc aag atg ccc Ala His Leu His Ser Asp His Thr Pro Cys Gly Arg Pro Lys Met Pro 360 365 370	1457
atc gtg cac agg gac ctc aag agc tcc aat atc ctc gtg aag aac gac Ile Val His Arg Asp Leu Lys Ser Ser Asn Ile Leu Val Lys Asn Asp 375 380 385 390	1505
cta acc tgc tgc ctg tgt gac ttt ggg ctt tcc ctg cgt ctg gac cct Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu Ser Leu Arg Leu Asp Pro 395 400 405	1553
act ctg tct gtg gat gac ctg gct aac agt ggg cag gtg gga act gca Thr Leu Ser Val Asp Asp Leu Ala Asn Ser Gly Gln Val Gly Thr Ala 410 415 420	1601
aga tac atg gct cca gaa gtc cta gaa tcc agg atg aat ttg gag aat Arg Tyr Met Ala Pro Glu Val Leu Glu Ser Arg Met Asn Leu Glu Asn 425 430 435	1649
gct gag tcc ttc aag cag acc gat gtc tac tcc atg gct ctg gtg ctc Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr Ser Met Ala Leu Val Leu 440 445 450	1697
tgg gaa atg aca tct cgc tgt aat gca gtg gga gaa gta aaa gat tat Trp Glu Met Thr Ser Arg Cys Asn Ala Val Gly Glu Val Lys Asp Tyr 455 460 465 470	1745
gag cct cca ttt ggt tcc aag gtg cg <sup>g</sup> gag cac ccc tgt gtc gaa agc Glu Pro Pro Phe Gly Ser Lys Val Arg Glu His Pro Cys Val Glu Ser 475 480 485	1793
atg aag gac aac gtg ttg aga gat cga ggg cga cca gaa att ccc agc Met Lys Asp Asn Val Leu Arg Asp Arg Gly Arg Pro Glu Ile Pro Ser 490 495 500	1841
ttc tgg ctc aac cac cag ggc atc cag atg gtg tgt gag acg ttg act Phe Trp Leu Asn His Gln Gly Ile Gln Met Val Cys Glu Thr Leu Thr 505 510 515	1889
gag tgc tgg gac cac gac cca gag gcc cgt ctc aca gcc cag tgt gtg Glu Cys Trp Asp His Asp Pro Glu Ala Arg Leu Thr Ala Gln Cys Val 520 525 530	1937
gca gaa cgc ttc agt gag ctg gag cat ctg gac agg ctc tcg ggg agg Ala Glu Arg Phe Ser Glu Leu Glu His Leu Asp Arg Leu Ser Gly Arg 535 540 545 550	1985
agc tgc tcg gag gag aag att cct gaa gac ggc tcc cta aac act acc Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp Gly Ser Leu Asn Thr Thr 555 560 565	2033
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Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro  
35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln  
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro  
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr  
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile  
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys  
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn  
130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu  
145 150 155 160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu  
165 170 175

Gly Val Ala Ile Ser Val Ile Ile Phe Tyr Cys Tyr Arg Val Asn  
180 185 190

Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys  
195 200 205

Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg  
210 215 220

Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu  
225 230 235 240

Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala  
245 250 255

Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu  
260 265 270

Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys  
275 280 285

Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile  
290 295 300

Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln  
305 310 315 320

Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr  
325 330 335

Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser  
340 345 350

Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys  
355 360 365

Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn  
370 375 380

Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu  
385 390 395 400

Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser  
405 410 415

Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser  
420 425 430

Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr  
 435 440 445

Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val  
 450 455 460

Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu  
 465 470 475 480

His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly  
 485 490 495

Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met  
 500 505 510

Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg  
 515 520 525

Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu  
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